

1646  
RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/887,9771460  
SECTOR

DATE: 03/09/98

TIME: 14:52:15 04/20/98 #8

INPUT SET: S24076.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Wang, Wei  
Gish, Kurt C.  
Schall, Thomas J.  
Vicari, Alain P.  
Zlotnik, Albert

(ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS

(iii) NUMBER OF SEQUENCES: 19

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute  
(B) STREET: 901 California Avenue  
(C) CITY: Palo Alto  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94304-1104

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/887,977  
(B) FILING DATE: 03-JUL-1997  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/021,644  
(B) FILING DATE: 05-JUL-1996

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/028,329  
(B) FILING DATE: 11-OCT-1996

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.  
(B) REGISTRATION NUMBER: 34,090  
(C) REFERENCE/DOCKET NUMBER: DX0589K1

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/887,977DATE: 03/09/98  
TIME: 14:52:17

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47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: 650-852-9192  
49 (B) TELEFAX: 650-496-1200  
50  
51

52 (2) INFORMATION FOR SEQ ID NO:1:  
53

54 (i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 1034 base pairs  
56 (B) TYPE: nucleic acid  
57 (C) STRANDEDNESS: single  
58 (D) TOPOLOGY: linear  
59

60 (ii) MOLECULE TYPE: cDNA  
61  
62

63 (ix) FEATURE:  
64 (A) NAME/KEY: CDS  
65 (B) LOCATION: 94..525  
66  
67

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
69

70	AGGCTACAAG CAGGCACCAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT	60
71		
72	TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC	114
73	Met Lys Leu Trp Leu Phe Ala	
74	1 5	
75		
76	TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC	162
77	Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala	
78	10 15 20	
79		
80	CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA	210
81	Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys	
82	25 30 35	
83		
84	TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT	258
85	Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser	
86	40 45 50 55	
87		
88	GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA	306
89	Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val	
90	60 65 70	
91		
92	GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC	354
93	Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile	
94	75 80 85	
95		
96	TTG ACA GCT AGG AAA AGG CTA GTC CAC TGG AAG AGC GCC TCA GAC TCT	402
97	Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser	
98	90 95 100	
99		

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100  CAG ACT GAA AGG AAG AAG TCA AAC CAT ATG AAG TCC AAG GTG GAG AAC      450
101  Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn
102      105                      110                      115
103
104  CCC AAC AGT ACA AGC GTG AGG AGT GCC ACC CTA GGT CAT CCC AGG ATG      498
105  Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met
106  120                      125                      130                      135
107
108  GTG ATG ATG CCC AGA AAG ACC AAC AAT TAAGTTAATT ACTCAGAGTA      545
109  Val Met Met Pro Arg Lys Thr Asn Asn
110      140
111
112  AGCACCAGCT GGAGGATGGG CGGAGTCTGC TGAAGTGCTG TCTTCTAGGC ATGCCAGTGC      605
113
114  CAATGAACTC ACTGAAGCTA CAGTTTCTCTG TACAAGACCA GACCCACCAA CGTCTCAGCA      665
115
116  TGTACGAGGA AGGAACTACT GCGCTAAAGG CCCTCCCACT CACCAAGGAG CTATTGGCTA      725
117
118  TTGATGATTG CTGAGGGAAG GGAGTAATTT TTTTCTCTT TCTGAAGTGT GACTTGAGTA      785
119
120  AATTGCCCCAT AGTTCAGTAT ATAATCCCCA ACCTGTGCTC AGGCAAGCAA CCCTAATTAA      845
121
122  ATGCAATAGC CACATACAAA AGAAGAGGAT ATGAATAGTT TGGTAGGAGG GGCTTGTTAG      905
123
124  GAAGAAGACA TTAACAGGAG AGAGAGGAGC GAGAGGATAG TGAGTGTGTG AGAGTGCCTG      965
125
126  CACGTGTGAA ATGGTCAAAG AATTAAAAAA TAAAACTTA AAAAGCTATT AAAAAGTAAA      1025
127
128  AAAAAATAAA      1034
129
130
131  (2) INFORMATION FOR SEQ ID NO:2:
132
133      (i) SEQUENCE CHARACTERISTICS:
134          (A) LENGTH: 144 amino acids
135          (B) TYPE: amino acid
136          (D) TOPOLOGY: linear
137
138      (ii) MOLECULE TYPE: protein
139
140      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
141
142  Met Lys Leu Trp Leu Phe Ala Cys Leu Val Ala Cys Phe Val Gly Ala
143      1                      5                      10                      15
144
145  Trp Met Pro Val Val His Ala Gln Gly Ala Phe Glu Asp Cys Cys Leu
146      20                      25                      30
147
148  Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn
149      35                      40                      45
150
151  Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg
152      50                      55                      60

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153
154 Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
155 65 70 75 80
156
157 Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
158 85 90 95
159
160 Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His
161 100 105 110
162
163 Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
164 115 120 125
165
166 Thr Leu Gly His Pro Arg Met Val Met Met Pro Arg Lys Thr Asn Asn
167 130 135 140
168
169

```

## (2) INFORMATION FOR SEQ ID NO:3:

### (i) SEQUENCE CHARACTERISTICS:

```

172 (A) LENGTH: 1012 base pairs
173 (B) TYPE: nucleic acid
174 (C) STRANDEDNESS: single
175 (D) TOPOLOGY: linear
176

```

### (ii) MOLECULE TYPE: cDNA

### (ix) FEATURE:

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182 (A) NAME/KEY: CDS
183 (B) LOCATION: 117..566
184

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### (ix) FEATURE:

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186 (A) NAME/KEY: mat_peptide
187 (B) LOCATION: 186..566
188

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### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

191
192 TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCGGGGCAT CAGCTCCCTT GACCCAGTGG 60
193
194 ATATCGGTGG CCCCGTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC 116
195
196 ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC 164
197 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
198 -23 -20 -15 -10
199
200 TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG 212
201 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
202 -5 1 5
203
204 GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT 260
205 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr

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206	10	15	20	25	
207					
208	TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA				308
209	Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile				
210		30	35	40	
211					
212	TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC				356
213	Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser				
214		45	50	55	
215					
216	AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT				404
217	Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val				
218		60	65	70	
219					
220	TTT GCA AAG CTC CAC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT				452
221	Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His				
222		75	80	85	
223					
224	GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG				500
225	Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys				
226		90	95	100	105
227					
228	TTT AGC AAT CCC ATC AGC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA				548
229	Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile				
230		110	115	120	
231					
232	TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTTCTGGG CTCCATCGGC				596
233	Ser Ala Asn Ser Gly Leu				
234		125			
235					
236	ACAGGAGGGG CCGGATCTTT CTCCGATAAA ACCGTCGCCC TACAGACCCA GCTGTCCCCA				656
237					
238	CGCCTCTGTC TTTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCCT CCCTCTGCAC				716
239					
240	CCCCACCACC TCCTGCCCCGT CTGGCAACTG GAAAGAAGGA GTTGGCCTGA TTTTAACCTT				776
241					
242	TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGTAG AGAAAACTTA				836
243					
244	GGATACCTCT CTCACTTTCT GTTTCTTGCC GTCCACCCCG GGCCATGCCA GTGTGTCTCTC				896
245					
246	TGGGTCCCCT CCAAAAATCT GGTCATTCAA GGATCCCCTC CCAAGGCTAT GCTTTTCTAT				956
247					
248	AACTTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAAAA AAAAAA				1012
249					
250					

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/887,977**

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*INPUT SET: S24076.raw*

Line

Error

Original Text